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REMARKS

The Title of the invention has been amended for clarity.

References to SEQ ID NOs: 7, 8, 9 and 10 have been replaced with SEQ ID NOs: 9, 10, 13 and 14 respectively. The amendments correct the references to amino acid and nucleic acid sequences, as set forth in the Sequence Listing. Sequence numbering is now consistent throughout the specification.

The amendments to pages 6 and 30 correct clerical errors. The amendments are supported at Figure 1.

The amendments to pages 23, 27, 29 and 33 correct typographical errors.

The amendment to page 32 corrects a typographical error. The amendment is supported at Figure 2, which shows 33 positions of identity out of a total of (approximately) 100 residues, among the amino acid sequences of the P11 proteins of ARV-138, ARV-176 and NBV.

Claims 5 to 28 have been amended for further clarity and to correct the references to amino acid and nucleic acid sequences, as set forth in the Sequence Listing.

Applicant points out that this is the first time that fusion-inducing proteins have been discovered in nonenveloped viruses and represent a novel class of fusion proteins. Therefore, the claimed proteins and methods recite the feature that the protein is encoded by, or is related to, the genome of *Reoviridae*. As claimed, the proteins of the present invention are distinguished from known fusion proteins, notably those of enveloped viruses.

With respect to new claims 43 to 45 and 49 to 52, proteins related to those encoded by *Reoviridae* are defined by the functional characteristic that the proteins have membrane fusion activity and by two structural characteristics: a minimum 33% amino acid sequence homology to the protein encoded by the genome of *Reoviridae* and a transmembrane domain. The defining feature "33% amino acid sequence identity" is supported at page 32, line 6, as corrected above. The relationship among the amino acid sequences of the P11 proteins of ARV-138, ARV-176 and NBV is such that a minimum of 33% homology sufficiently defines the variant, and is within the scope of the

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invention as long as the variant contains a transmembrane domain and has membrane fusion activity. Fusion activity can be readily detected by applying a simple test, such as that exemplified in Example 4 (page 28 of the specification).

New claims 46 and 53 recite *"a cluster of positive amino acid residues, wherein the cluster is located on the C-terminal side of the transmembrane domain and comprises at least 4 positive residues within the 20 residues flanking the transmembrane domain at the C-terminal side"*. These claims are supported at least at page 32, lines 16 to 20, as well as Figure 2. The expression "at least" is supported by Figure 2, which shows that there may be positive residues (K, R and possibly H) within the cluster in addition to the 6 residues of the consensus sequence.

New claims 47 and 54 recite that the protein *"lacks a signal peptide"*. This feature is supported at least by claim 1 and Example 7.

New claims 48 and 55 recite *"4 cysteine residues at conserved positions relative to SEQ ID NO:2 (ARV1); SEQ ID NO:6 (ARV2); and SEQ ID NO:10 (NBV)"*. Support for this feature is found at least at page 32, lines 20 to 23, as well as Figure 2.

New claim 56 is supported at least at claim 2.

New claim 57 is supported at least at claim 4 and, as explained above, the claim recites the feature that the protein is encoded by a polynucleotide from the genome of *Reoviridae*.

New claim 58 to 77 are drawn to methods of using fusogenic proteins of *Reoviridae* or related proteins to fuse membranes. The claims are supported throughout the specification and the claims as originally filed.

Attached hereto is a marked-up version of the changes made to the specification and claims. The attached page is captioned **"Version with markings to show changes made"**.

No new matter is introduced by the amendments or by the new claims.

The Petition for Extension of Time pursuant to 37 CFR 1.136(a) and the fee have been submitted with our letters of June 29 and July 30, 2001. The

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U.S.P.T.O. is authorized to withdraw from our deposit account number 19-2550 any excess claims fees if required.

Respectfully submitted,

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In re Application

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

The Title paragraph beginning at page 1, line 1, has been amended as follows:

Novel Reovirus-derived Proteins, Nucleic Acids Encoding Same, Reovirus-Derived Proteins and Uses Therefor

The paragraph beginning at page 6, line 2, has been amended as follows:

Figure 1 collectively presents schematic diagrams of reovirus fusion protein-encoding genome segments. Thus, Figure 1A presents segments from ~~avian reovirus (ARV); Nelson bay virus (NBV);~~ Figure 1B presents segments from ~~Nelson bay virus~~avian reovirus (NBV); (ARV); and Figure 1C presents segments from Baboon Reovirus (BRV).

The paragraph beginning at page 7, line 7, has been amended as follows:

Exemplary proteins embraced by the above-described profile of properties include proteins having an amino acid sequence substantially the same as set forth in SEQ ID NO:2, proteins having an amino acid sequence substantially the same as set forth in SEQ ID NO:6, proteins having an amino acid sequence substantially the same as set forth in SEQ ID NO:8, NO:10, and the like.

The paragraph beginning at page 7, line 14, has been amended as follows:

Presently preferred proteins embraced by the above-described profile of properties include proteins having the same amino acid sequence as set forth in SEQ ID NO:2, proteins having the same amino acid sequence as set forth in SEQ ID NO:6, proteins having the same amino acid sequence as set forth in SEQ ID NO:8, NO:10, and the like.

The paragraph beginning at page 8, line 7, has been amended as follows:

Exemplary proteins embraced by the above-described profile of properties include proteins having an amino acid sequence substantially the same as set forth in SEQ ID NO:10. Presently preferred proteins embraced by the above-described profile of properties include proteins having the same amino acid sequence as set forth in SEQ ID NO:10, NO:14.

The paragraph beginning at page 10, line 29, has been amended as follows:

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Exemplary isolated nucleic acids contemplated for use in the practice of the present invention include nucleic acids having a contiguous nucleotide sequence substantially the same as:

nucleotides 25-1607 of SEQ ID NO:1,

nucleotides 25-1607 of SEQ ID NO:5,

nucleotides 27-1579 of SEQ ID NO:7, NO:9,

nucleotides 25-832 of SEQ ID NO:9, NO:13, or

variations thereof which encode the same amino acid sequence, but employ different codons for some of the amino acids, or splice variant nucleotide sequences thereof.

The paragraph beginning at page 11, line 11, has been amended as follows:

Presently preferred isolated and purified nucleic acids, or functional fragments thereof contemplated according to the invention are nucleic acids encoding the above-described proteins, e.g.,

(a) DNA encoding the amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8 or SEQ ID NO:10, NO:10 or SEQ ID NO:14, or

(b) DNA that hybridizes to the DNA of (a) under moderately stringent conditions, wherein said DNA encodes biologically active fusion protein, or

(c) DNA degenerate with respect to either (a) or (b) above, wherein said DNA encodes biologically active fusion protein.

The paragraph beginning at page 11, line 24, has been amended as follows:

As employed herein, the term "contiguous nucleotide sequence substantially the same as" refers to DNA having sufficient homology to the reference polynucleotide, such that it will hybridize to the reference nucleotide under typical stringency conditions employed by those of skill in the art. In one embodiment, DNA having substantially the same nucleotide sequence as the reference nucleotide encodes substantially the same amino acid sequence of SEQ ID NOs:2, 6, 8, 10 or 14. In another embodiment, DNA having "a contiguous nucleotide sequence substantially the same as" has at least 60% homology with respect to the nucleotide

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sequence of the reference DNA fragment with which the subject DNA is being compared. In a preferred embodiment, the DNA has at least 70%, more preferably 80%, homology to the comparative nucleotide sequence; with greater than about 90% homology being especially preferred.

The paragraph beginning at page 14, line 8, has been amended as follows:

As used herein, a nucleic acid "probe" is single-stranded DNA or RNA, or analogues thereof, that has a sequence of nucleotides that includes at least 14, preferably at least 20, more preferably at least 50, contiguous bases that are the same as (or the complement of) any 14 or more contiguous bases set forth in any of SEQ ID NOs:1, 5, 79 or 9-13. Probes may be labeled by methods well-known in the art, as described hereinafter, and used in various diagnostic kits.

The paragraph beginning at page 23, line 6, has been amended as follows:

The detergent-protein complexes can be mixed with lipids and the detergent removed by dialysis, chromatography, or extraction according to standard published procedures, similar to methods used to generate influenza HA or Sendai virus F protein-containing virosomes (see Grimaldi, *Res. Virol.*, 146:289-293 (1995) and Ramani et al., *FEBS Lett.*, 404:164-168 (1997)). These procedures will result in the production of proteoliposomes, lipid vesicles containing the ARV, NBV, or BRV fusion proteins embedded in the vesicle membrane. Once again, optimal conditions for proteoliposome production can be empirically determined as can the lipid composition and size of the proteoliposomes which can affect the efficiency of liposome-cell fusion. Bioactive molecules of interest (e.g., nucleic acids, proteins or peptides, pharmacological compounds, and the like) can be included during the formation of the proteoliposomes to facilitate packaging of the molecule within the liposomes. The proteoliposomes can be purified by centrifugation and used to deliver bioactive molecules intracellularly, either in cell culture or *in vivo*, by protein-enhanced fusion of the proteoliposomes with cell membranes.

The paragraph beginning at page 27, line 13, has been amended as follows:

The two strains of ARV were grown in monolayers of QM5 cells, a continuous quail cell line (see Antin and Ordahl, *Devel. Biol.*, 143:111-121 (1991)) while the fusogenic mammalian reoviruses were grown in monkey Vero cells. Virus particles were isolated and concentrated from infected cell lysates by differential centrifugation, as previously described (see Duncan, *Virology*, 219:179-189 (1996)).

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Two unrelated fusion proteins responsible for the cell-cell fusion induced by avian reovirus (ARV) and the only two fusogenic mammalian reoviruses, Nelson Bay virus (NBV) and baboon reovirus (BRV) have been identified. These proteins are referred to herein as P11 (for ARV and NBV) and P15 (for BRV) to reflect their approximate predicted molecular weights. The genes encoding P11 from two strains of ARV (strain 176 and strain 138) and from NBV have been cloned and sequenced, as has the gene from NBVBRV that encodes P15. The sequence-predicted structural organization of these proteins has been analyzed, and the membrane fusion properties thereof have been directly demonstrated.

The paragraph beginning at page 33, line 24, has been amended as follows:

The fusion-inducing potential of these reovirus proteins has been directly demonstrated by expressing them in transfected cells in the absence of any other reovirus proteins; intracellular expression triggers the induction of cell-cell fusion and syncytium formation characteristic of virus infection by this group of fusogenic reoviruses. Thus, quail cell monolayers were mock transfected, or transfected with plasmid DNA expressing the ARV, BRV, or NBV fusion proteins. Transfected cells were fixed and the nuclei stained using a Wright-Giemsa stain at 36 hr post infection and the stained monolayers were photographed at 100x magnification.

The paragraph beginning at page 32, line 6, has been amended as follows:

The ARV and NBV P11 proteins are small proteins (98 or 95 amino acids, respectively) that share approximately 38% sequence homology and a similar domain organization indicating that these proteins are evolutionarily related (Figure 2). Both proteins lack obvious signal peptides, suggesting that they insert in membranes post-translationally. Both proteins also contain one predicted transmembrane domain located in the central portion of the protein resulting in small (approximately 40 amino acid) intracellular and extracellular domains. The conserved clustering of positively charged amino acids on the carboxy-proximal side of the transmembrane domain is consistent with the amino-terminal domain residing extracellularly (von Heijne, *Curr. Op. Cell Biol.*, 2:604-608 (1990)). The four cysteine residues in each protein are conserved, suggesting that the ARV and NBV P11 proteins assume a similar tertiary and quaternary structure. The ARV P11 protein is devoid of N-linked glycosylation sites, implying that post-translational glycosylation is not required for functional protein folding, a prediction that has been confirmed experimentally (see Duncan et al. (1996), *supra*). Although the NBV P11 protein contains a single potential N-linked glycosylation site, this site is probably not glycosylated since inhibitors of glycosylation fail to affect NBV-induced cell fusion (see Wilcox and Compans (1983)). The size, absence of signal peptides, and N-linked glycosylation, and predicted domain organization of the ARV and NBV P11 proteins clearly distinguishes these proteins from the well characterized enveloped virus fusion proteins and suggests that P11 represents a novel type of membrane fusion protein.

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In the Claims:

Claims 5 to 28 have been amended as follows:

5. ~~A protein according to~~[Amended] The protein of claim 4 having an amino acid sequence substantially the same as set forth in SEQ ID NO-10NO: 14 [BRV].
6. ~~A protein according to~~[Amended] The protein of claim 4 having the amino acid sequence set forth in SEQ ID NO: 1014 [BRV].
7. [Amended] An antibody raised against the protein of claim 1-43.
8. [Amended] An antibody raised against the protein of claim 4.
9. [Amended] An isolated nucleic acid encoding protein according to claim 1-the protein of claim 43.
10. [Amended] An isolated nucleic acid according to claim 9 having a contiguous nucleotide sequence substantially the same as:
nucleotides 25-1607 of SEQ ID NO: 1 [ARV1],
nucleotides 25-1607 of SEQ ID NO: 5 [ARV2],
nucleotides 27-1579 of SEQ ID NO: 79 [NBV], or
variations thereof which encode the same amino acid sequence, but employ different codons for some of the amino acids, or splice variant nucleotide sequences thereof.
11. [Amended] An isolated and purified nucleic acid, or functional fragment thereof encoding the protein of claim 1-43, wherein the nucleic acid is selected from the group consisting of:
(a) DNA encoding the amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 6 or SEQ ID NO: 8,10, or
(b) DNA that hybridizes to the DNA of (a) under moderately stringent conditions, wherein said DNA encodes a biologically active fusion protein, or
(c) DNA degenerate with respect to either (a) or (b) above, wherein said DNA encodes a biologically active fusion protein.
12. [Amended] An isolated nucleic acid according to claim 9 operatively associated with an inducible promoter.

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13. [Amended] An isolated nucleic acid encoding protein according to the protein of claim 4.

14. ~~An~~[Amended] The isolated nucleic acid according to claim 13 having a contiguous nucleotide sequence substantially the same as:

nucleotides 25-832 of SEQ ID NO: 913 [BRV], or

variations thereof which encode the same amino acid sequence, but employ different codons for some of the amino acids, or splice variant nucleotide sequences thereof.

15. [Amended] An isolated and purified nucleic acid, or functional fragment thereof encoding the protein of claim 4, wherein the nucleic acid is selected from the group consisting of:

(a) DNA encoding the amino acid sequence set forth in SEQ ID NO: 10, 14, or

(b) DNA that hybridizes to the DNA of (a) under moderately stringent conditions, wherein said DNA encodes a biologically active fusion protein, or

(c) DNA degenerate with respect to either (a) or (b) above, wherein said DNA encodes a biologically active fusion protein.

16. ~~An~~Amended The isolated nucleic acid according to claim 13 operatively associated with an inducible promoter.

17. ~~Cells containing protein according to claim 1.~~

- ~~18. Cells containing protein according to claim 4.~~

- ~~19. Cells containing nucleic acid according to claim 9.~~

- ~~20. Cells containing nucleic acid according to claim 12.~~

- ~~21. Cells containing nucleic acid according to claim 13.~~

- ~~22. Cells containing nucleic acid according to claim 16.~~

- ~~23. Liposomes containing protein according to claim 1.~~

- ~~24. Liposomes containing protein according to claim 4.~~

- ~~25. Liposomes containing nucleic acid according to claim 9.~~

26. ~~Liposomes containing nucleic acid according to~~[Amended] A cell containing the protein of claim 43.

18. [Amended] The cell containing the protein of claim 4.

19. [Amended] The cell containing the nucleic acid of claim 9.

20. [Amended] The cell containing the nucleic acid of claim 12.

21. [Amended] The cell containing the nucleic acid of claim 13.

22. [Amended] The cell containing the nucleic acid of claim 16.

23. [Amended] Liposomes containing the protein of claim 43.

24. [Amended] Liposomes containing the protein of claim 4.

25. [Amended] Liposomes containing the nucleic acid of claim 9.

26. [Amended] Liposomes containing the nucleic acid of claim 13.

27. ~~A method for the production of protein according to claim 1, said method comprising expressing~~[Amended] A method for producing the protein of claim 43, said method comprising the step of expressing a nucleic acid encoding said protein in a suitable host.

28. ~~A method for the production of protein according to~~[Amended] A method for producing the protein of claim 4, said method comprising the step of expressing a nucleic acid encoding said protein in a suitable host.

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